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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2011; month=3; day=22; hr=10; min=46; sec=25; ms=118;]
=====

Reviewer Comments:

<210> 2
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> modified NS5B

(ERRORED PORTION SHOWN BELOW)

<221> variation
<222> (83)...(83)
<223> n = G or T

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ttaccgatca nccctctgag taattcgctc atncgggttcc ataataaggt gtactccaca 120

The above "<220>-<223>" section describing the "n" at location 83 is
errored: "a" is at that location. The "n" at location 93 is not
explained above.

<210> 4
<211> 4182
<212> DNA
<213> Artificial Sequence

<220>
<223> modified NS3-5A

<221> variation
<222> (2711)...(2711)
<223> n = T or C

<221> variation
<222> (3645)...(3645)
<223> n = A or G

(ERRORED PORTIONS SHOWN BELOW)

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ggtaatcatg tttccccccac gcactatgtg cctgagagcg acgccgcagc gcgtgttact 2760

There is no "n" at location 2711: "t" is at that location.

ttgtctgcgc cttccttgaa ggcgacatgc actaccacc atgtctctcc ggacgctgac 3600
ctcatcgagg ccaacctcct gtggcggcag gagatgggcg ggancatcac ccgcgtggag 3660

There is no "n" at location 3645: "c" is at that location. The "n" at
location 3644 is not explained above.

Application No: 10577893 Version No: 1.0

Input Set:**Output Set:**

Started: 2011-03-11 10:24:53.976
Finished: 2011-03-11 10:24:56.181
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 205 ms
Total Warnings: 28
Total Errors: 2
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 342	'n' position not defined found at POS: 93 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 342	'n' position not defined found at POS: 3644 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

Input Set:

Output Set:

Started: 2011-03-11 10:24:53.976
Finished: 2011-03-11 10:24:56.181
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 205 ms
Total Warnings: 28
Total Errors: 2
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Ludmerer, Steven W.
 Graham, Donald J.
 LaFemina, Robert L.
 Flores, Osvaldo A.
 Pizzuti, Maura
 Traboni, Cinzia

<120> HCV REPLICONS CONTAINING NS5B FROM
 GENOTYPE 2B

<130> 21564YP

<140> 10577893
 <141> 2011-03-11

<150> PCT/US2004/036575
 <151> 2004-11-03

<150> 60/517,605
 <151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

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 <222> (5)...(5)
 <223> Xaa = threonine or serine

<221> VARIANT
 <222> (24)...(24)
 <223> Xaa = asparagine or serine

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa = methionine or isoleucine

<221> VARIANT
 <222> (392)...(392)
 <223> Xaa = isoleucine or leucine

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Arg	Leu	Leu	Thr	Val	Glu	Glu	Ala	Cys	Ala	Leu	Thr	Pro	Pro	His	Ser	
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	130					135					140					
Phe	Cys	Ile	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Pro	Ala	Arg	Leu	Ile	
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Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr	
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Gln	Ala	Cys	Ser	Leu	Pro	Gln	Glu	Ala	Arg	Thr	Val	Ile	His	Ser	Leu	
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			325						330					335		
Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	Asp	
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Tyr	His	Ser	Val	Ser	His	Ala	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Cys	Leu
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (3)...(3)
 <223> n = A or T

<221> variation
 <222> (9)...(9)
 <223> n = C or A

<221> variation
 <222> (13)...(13)
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 <222> (15)...(15)
 <223> n = A or C

<221> variation
 <222> (21)...(21)
 <223> n = A or G

<221> variation
 <222> (24)...(24)
 <223> n = C or G

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 <223> n = T or C

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 <223> n = G or C

<221> variation

<222> (33)...(33)

<223> n = C or A

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<222> (71)...(71)

<223> n = A or G

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<222> (83)...(83)

<223> n = G or T

<221> variation

<222> (1174)...(1174)

<223> n = A or C

<400> 2

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cggtacttcc taaccagaga ccctaccact ccantcacc gagctgcttg ggaaacagta 1200
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<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS3-5A

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<222> (1215)...(1215)

<223> Xaa = asparagine or serine

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<223> Xaa = valine or alanine

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Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp
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Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr
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Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala
			100					105					110		
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu
		115					120					125			
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu
	130					135					140				
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys
145					150					155					160
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met
				165					170					175	
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro
			180					185					190		
Ala	Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly
		195					200					205			
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr
	210					215					220				
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly
225					230					235					240
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly
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Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly
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Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn
				325					330					335	
Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly
			340					345					350		
Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe
		355					360					365			
Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly
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Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val
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				420				425					430			
Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	
				435				440				445				
Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	
				450			455				460					
Arg	Thr	Gly	Arg	Gly	Arg	Met	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	
465					470					475					480	
Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	
				485				490					495			
Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	
				500				505					510			
Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	
				515			520					525				
His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	
				530			535				540					
Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	
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Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	
				565					570					575		
Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	
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Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	
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				610			615				620					
Ser	Ala	Asp	Leu	Glu	Val	Val	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	
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Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	
				645					650					655		
Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Ile	Val	Pro	Asp	
				660				665					670			
Arg	Glu	Phe	Leu	Tyr	Gln	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	
				675			680					685				
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	
				690			695					700				
Gln	Lys	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	
705					710					715					720	
Ala	Ala	Pro	Val	Val	Glu	Ser	Lys	Trp	Arg	Ala	Leu	Glu	Thr	Phe	Trp	
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Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	
				740				745					750			
Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	
				755			760					765				
Thr	Ala	Ser	Ile	Thr	Ser	Pro	Leu	Thr	Thr	Gln	Ser	Thr	Leu	Leu	Phe	
				770			775					780				
Asn	Ile	Leu	Gly	Gly	Trp	Val	Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala	
785					790					795					800	
Ala	Ser	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser	
				805					810					815		
Ile	Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	
				820				825				830				
Gly	Val	Ala	Gly	Ala	Leu	Val	Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Met	
				835			840					845				
Pro	Ser	Thr	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	

850		855		860	
Gly	Ala	Leu	Val	Val	Gly
865		870		875	880
Val	Gly	Pro	Gly	Glu	Gly
		885		890	895
Phe	Ala	Ser	Arg	Gly	Asn
		900		905	910
Ser	Asp	Ala	Ala	Ala	Arg
		915		920	925
Thr	Gln	Leu	Leu	Lys	Arg
		930		935	940
Thr	Pro	Cys	Ser	Gly	Ser
945		950		955	960
Thr	Val	Leu	Thr	Asp	Phe
		965		970	975
Gln	Leu	Pro	Gly	Val	Pro
		980		985	990
Val	Trp	Arg	Gly	Asp	Gly
		995		1000	1005
Gln	Ile	Thr	Gly	His	Val
		1010		1015	1020
Lys	Thr	Cys	Ser	Asn	Thr
1025		1030		1035	1040
Thr	Thr	Gly	Pro	Cys	Thr
		1045		1050	1055
Leu	Trp	Arg	Val	Ala	Ala
		1060		1065	1070
Asp	Phe	His	Tyr	Val	Thr
		1075		1080	1085